Systematic evaluation of the impact of involuntary motion in whole body dynamic PET

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***Abstract*—Involuntary patient motion can happen in dynamic whole body (DWB) PET due to long scanning times, which may cause inaccurate quantification of tissue parameters. To quantify the impact on Patlak parameters, we simulated dynamic data using patient-derived motion fields, systematically introducing the motion at different passes of the dynamic scan, both inter and intra-frame. Estimated parameters are compared against the ground truth. Results show that errors can be large, even for small motion. Caution is advised when quantitatively evaluating DWB-PET images, if any motion has been detected.**

***Index Terms*—dynamic whole body PET, simulation, Patlak**

I. Introduction

Dynamic whole body positron emission tomography (DWB-PET) is a promising technique that can improve quantification and assessment of systemic diseases[1], tumor diagnosis and characterization[2]. This is achieved by estimating parametric images of the tracer uptake rate constant, which comes with many technical challenges. Among others involuntary patient motion, prominent due to the long scanning times required, can hinder correct quantitative parametric image reconstruction. Although motion in PET is a well–studied problem, most of the literature concentrates on respiratory motion or rigid motion usually limited to the brain.

In this work, we use simulation tools to study whole-body involuntary motion, e.g. due to patient discomfort over the acquisition period, and in particular its effect on parametric tumour quantification. Arm motion was investigated in [3], concluding that its effect can be limited by adjusting the scatter scaling. Common motion types in cardiac PET patients were identified in [4] and simulated with simplified motion models, showing that parametric images can be severely misquantified in the presence of motion, particularly if the motion happens at mid or late frame.

In this work, we build a simulation pipeline that uses patient derived motion applied at different time frames to systematically evaluate the impact of motion on Patlak parametric images.

II. Methods

The simulation pipeline consists of dynamic PET simulation and reconstruction, while using motion derived from clinical exams. For all the following work, the SIRF open source package [5] has been used.

A. Clinical data

The clinical data consists of dynamic whole body scans of 8 different patients, acquired on a GE Discovery MI (DMI) at University Hospital Zurich, Switzerland. The exam starts with 10 to 15 minutes positioned over the heart to acquire an image derived input function (IF) and a subsequent $6-10$ whole body passes of 35 seconds per bed position, depending on the patient. For all, 60 minutes after the injection an SUV image was acquired. A CTAC was acquired before injection time. Each whole body pass was reconstructed using the standard reconstruction technique for the DMI. For this work, patients that show visible motion during the scanning process have been selected.

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B. Patient-derived motion

Patient motion is obtained for each patient and frame by registering it with non-rigid transformation into their corresponding first WB dynamic pass (this frame is closest to the CTAC acquisition). This work uses the fast free-form B-spline deformation algorithm with normalized mutual information as objective function, as implemented in NiftyReg [6]. The registration was moderately over-regularized by applying a sparse 15 voxel space between B-spline control points, to ensure that sharp yet localized movements do not dominate the registration such that gross body movement was recovered.

C. Simulations

A series of dynamic scans following the clinical DWB-PET protocol were generated using the XCAT phantom [7], assigning patient-derived kinetic parameters to 64 tissues and 3 tumours of 1 cm diameter in the left lung, and 3 tumours of 2.5 cm, 2 cm and 1 cm diameter in the liver [8]. An input function for 18F-FDG taken from [9] was used to simulate time activity curves (TACs) to create dynamic images.

The simulated images were registered to images in 2 positions: the patient's CTAC, and the position of the patient at the SUV image stage (last frame of the dynamic scan).

Two types of simulated motion were then introduced for the dynamic data: step-like and impulse-like motion. Step-like motion uses dynamic images from a single position until, at a specified frame, the patient position is changed. Alternatively, impulse-like motion introduces a single moved frame. Both of these experiments were run over the 14 frames of the dynamic simulation and motion was systematically introduced in each of the frames. For step-like motion, intraframe motion is also simulated, where the patient moves mid-frame.

Non-TOF sinogram data were simulated using resolution modelling (using a 6 cm FWHM Gaussian filter), and using the repositioned attenuation maps. Randoms and scatter were not included.

Finally, all datasets were reconstructed using 10 iterations with 17 subsets of OSEM, with the attenuation map fixed at

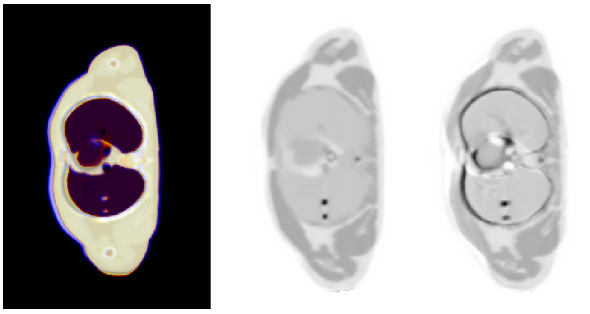

Fig. 1. Left: Composite image of CT XCAT phantom registered to first and last dynamic frame of patient A. Middle: reconstructed time frame at SUV time without motion or attenuation mismatch. Right: the same time frame with motion and attenuation mismatch

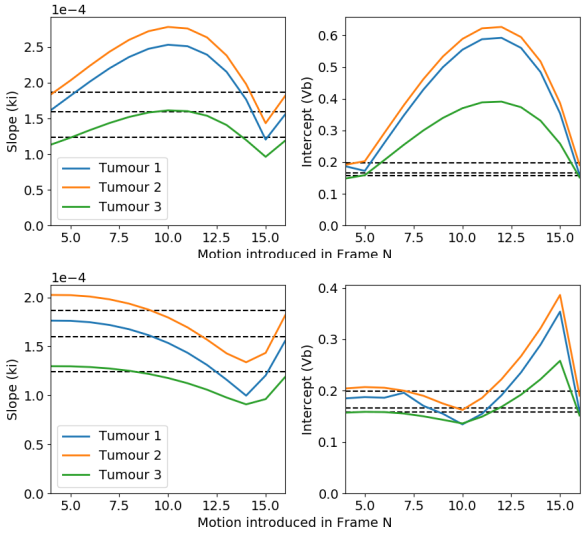

Fig. 2. Patlak slope (K_i) and intercept (V_b) value (SUV_{peak}) against frame where step-like motion (top) and impulse-like motion (bottom) was introduced, for tumours in the liver using motion from patient A. The dashed line shows the correct values of the tumour, for a simulation without motion.

the first (CTAC) position. See Figure 1 for an illustration of the motion and the impact of the attenuation mismatch in a single time frame. We noticed that the mismatch of the AC generates $5-10\%$ error on concentration values when the mismatch is large.

For each of the parametric Patlak images, each tumour's slope and intercept were quantified using ROI_{max}, ROI_{peak} (as per EANM guideline for SUV_{peak} [10]) and ROI_{mean} (by thresholding at 42% of the maximum value and averaging).

III. Results

As all quantitative measures show a similar behaviour, only results of SUV_{peak} are presented. Figure 2 shows the change of value on the slope and intercept against the frame number where the motion was introduced in the indirect Patlak reconstruction. Intraframe motion (not shown) follows the same curve.

General analysis of motion is not trivial, as the patient derived motion is different for each patient in form and magnitude. In Figure 3 the percentage change in K_i of each tumour in the liver and lung in all patients is shown, plotted

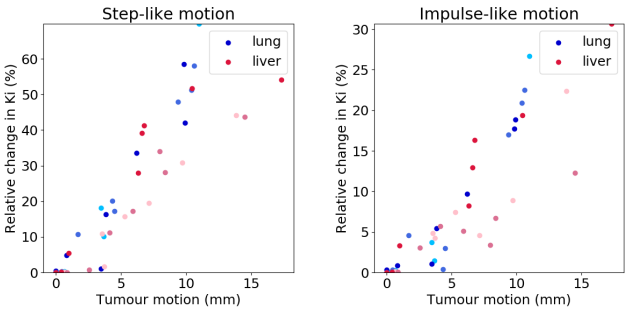

Fig. 3. Relative change of SUV_{peak} vs motion in the tumour, for step-like motion (left) and impulse-like motion (right). This plot is for motion introduced at frame 10 for step size motion and frame 16 for impulse-like motion, as it is the point where the differences were largest (see Figure 2).

against the average motion in mm of each tumour. Similar behaviour was obtained at other time frames, but with smaller error. For reference, the pixel size is $2.2 \times 2.2 \times 2.76$ mm.

IV. Discussion and Conclusions

Results suggest that even small amounts of motion can lead to large changes in tumour quantification. Patlak estimation has been shown to amplify errors caused by attenuation mismatch [11], and simulation presented here show that it also amplifies motion artifacts greatly. Albeit impulse-like motion simulation shows a more moderate misquantification of tumour values, it is higher than 10% when the tumour moves around 5 mm (50% of its size for the lung), this motion mode is expected to be less representative of the clinic, as patients are unlikely to come back to their original position with millimeter precision. Future work will include studying the impact on direct Patlak reconstruction and looking at line fitting residuals as motion markers, with more patient data.

The presented results reinforce that motion correction is a key factor in quantitative PET analysis, and that accurate methods for motion detection, modelling and correction are essential for intra- and inter-patient dynamic PET studies.

References

[1] A. Rahmim *et al.*, eng, *Eur. J. Nucl. Med. Mol. Imaging*, 2019. DOI: 10.1007/s00259-018-4153-6.

[2] A. Dimitrakopoulou-Strauss, L. Pan, and C. Sachpekidis, en, *Eur. J. Nucl. Med. Mol. Imaging*, 2021. DOI: 10.1007/s00259-020-04843-6.

[3] M. A. Lodge *et al.*, en, *J. Nucl. Med.*, 2011. DOI: 10.2967/jnumed.111.093583.

[4] C. R. R. N. Hunter *et al.*, en, *Med. Phys.*, 2016, _eprint: https://aapm.onlinelibrary.wiley.com/doi/pdf/10.1118/1.4943565. DOI: https://doi.org/10.1118/1.4943565.

[5] E. Ovtchinnikov *et al.*, *Computer Physics Communications*, 2020. DOI: https://doi.org/10.1016/j.cpc.2019.107087.

[6] M. Modat *et al.*, eng, *Comput. Meth. Prog. Bio.*, 2010. DOI: 10.1016/j.cmpb.2009.09.002.

[7] W. P. Segars *et al.*, eng, *Med. Phys.*, 2010. DOI: 10.1118/1.3480985.

[8] G. Wu *et al.*, English, *Cancer. Manag. Res.*, 2018, Publisher: Dove Press. DOI: 10.2147/CMAR.S177663.

[9] J. W. Långsjö *et al.*, eng, *Anesthesiology*, 2004. DOI: 10.1097/00000542-200405000-00006.

[10] R. Boellaard *et al.*, *Eur. J. Nucl. Med. Mol. Imaging*, 2015.

[11] B. F. Holman *et al.*, *Phys. Med. Biol.*, 2016. DOI: 10.1088/0031-9155/61/8/3148.